

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gregory Plowman  
Douglas Clary

(ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
Alk-7 RELATED DISORDERS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon  
(B) STREET: 633 West Fifth Street  
Suite 4700  
(C) CITY: Los Angeles  
(D) STATE: California  
(E) COUNTRY: U.S.A.  
(F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0  
(D) SOFTWARE: FastSEQ for Windows 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Filed herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/044,428  
(B) FILING DATE: April 28, 1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warburg, Richard J.  
(B) REGISTRATION NUMBER: 32,327  
(C) REFERENCE/DOCKET NUMBER: 234/118

(ix) TELECOMMUNICATION INFORMATION:

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(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGCCACACT	GAATAGAGCC	AACCGCGCAC	TTCAAAAGGG	TGTCGGTGCC	GCGCTCCCT	60
CCC CGGGCCC	GGGAACCTCA	AAGCGGGCCG	TGCTGCCCG	GCTGCCTCGC	TCTGCTCTGG	120
GGCCTCGCAG	CCCCGGCGCG	GCCGCCCTGGT	GGCGATGACC	CGGGCGCTCT	GCTCAGCGCT	180
CGGCCAGGCT	CTCCTGCTGC	TCGCAGGGC	CGCCGAGCTC	TGCGCAGGAC	TGAAGTGTGT	240
ATGTCTTTG	TGTGATTCTT	CAAACTTAC	CTGCCAAACA	GAAGGAGCAT	GTTGGGCATC	300
AGTCATGCTA	ACCAATGGAA	AAGAGCAGGT	GATCAAATCC	TGTGTCTCC	TTCCAGAACT	360
GAATGCTCAA	GTCTTCTGTC	ATAGTTCCAA	CAATGTTACC	AAAACGAAAT	GCTGCTTCAC	420
AGATTTTGC	AACAAACATAA	CACTGCACCT	TCCAACAGCA	TCACCAAATG	CCCCAAAAC	480
TGGACCCATG	GAGCTGGCCA	TCATTATTAC	TGTGCCCTGTT	TGCCTCCTGT	CCATAGCTGC	540
GATGCTGACA	GTATGGGCAT	GCCAGGGTCG	ACAGTGCTCC	TACAGGAAGA	AAAAGAGACC	600
AAATGTGGAG	GAACCACTCT	CTGAGTGCAA	TCTGGTAAAT	GCTGGAAAAA	CTCTGAAAGA	660
TCTGATTTAT	GATGTGACCG	CCTCTGGATC	TGGCTCTGTT	CTACCTCTGT	TGGTTCAAAG	720
GACAATTGCA	AGGACGATTG	TGCTTCAGGA	AATAGTAGGA	AAAGGTAGAT	TTGGTGAGGT	780
GTGGCATGGA	AGATGGTGTG	GGGAAGATGT	GGCTGTGAAA	ATATTCTCCT	CCAGAGATGA	840
AAGATCTTGG	TTTCTGTGAGG	CAGAAATTTA	CCAGACGGTC	ATGCTGCGAC	ATGAAAACAT	900
CCTTGGTTTC	ATTGCTGCTG	ACACAAAGAA	TAATGGAACT	TGGACTCAAC	TTGGCTGGT	960
ATCTGAATAT	CATGAACAGG	GCTCCTTATA	TGACTATTG	AATAGAAATA	TAGTGACCGT	1020
GGCTGGAATG	ATCAAGCTGG	CGCTCTCAAT	TGCTAGTGGT	CTGGCACACC	TTCATATGGA	1080
GATTGTTGGT	ACACAAGGTA	AACCTGCTAT	TGCTCATCGA	GACATAAAAT	CAAAGAATAT	1140
CTTAGTGAAA	AAGTGTGAAA	CTTGTGCCAT	AGCGGACTTA	GGGTTGGCTG	TGAAGCATGA	1200
TTCAATACTG	AACACTATCG	ACATACCTCA	GAATCCTAAA	GTGGGAACCA	AGAGGTATAT	1260
GGCTCCTGAA	ATGCTTGATG	ATACAATGAA	TGTGAATATC	TTTGAGTCCT	TCAAACGAGC	1320
TGACATCTAT	TCTGTTGGTC	TGGTTTACTG	GGAAATAGCC	CGGAGGTGTT	CAGTCGGAGG	1380
AATTGTTGAG	GAGTACCAAT	TGCCTTATTA	TGACATGGTG	CCTTCAGATC	CCTCGATAGA	1440
GGAAATGAGA	AAGGTTGTTT	GTGACCAGAA	GTTTCGACCA	AGTATCCCAA	ACCAGTGGCA	1500
AAGTTGTGAA	GCACCTCGAG	TCATGGGGAG	AATAATGCGT	GAGTGTGTT	ATGCCAACGG	1560
AGCGGGCCCG	CTAACTGCTC	TTCGTATTAA	GAAGACTATA	TCTCAACTT	GTGCAAAGA	1620
AGACTGCAA	GCCTAATGAT	GATAATTATG	TTAAAAGAA	ATCTCTCATA	GCTTTCTTT	1680
CCATTTTCCC	CTTTATGTGA	ATGTTTTGTC	CATTTTTTT	TTGTTCTACC	TCAAAGATAA	1740
GACAGTACAG	TATTAAGTG	CCCATAAGGC	AGCATGAAAA	GATAACTCTA	AAG	1793

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Thr	Arg	Ala	Leu	Cys	Ser	Ala	Leu	Arg	Gln	Ala	Leu	Leu	Leu	
1				5				10				15			
Ala	Ala	Ala	Ala	Glu	Leu	Ser	Pro	Gly	Leu	Lys	Cys	Val	Cys	Leu	Leu
				20				25				30			

Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala  
 35 40 45  
 Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val  
 50 55 60  
 Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn  
 65 70 75 80  
 Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr  
 85 90 95  
 Leu His Leu Pro Thr Ala Ser Pro Asn Ala Pro Lys Leu Gly Pro Met  
 100 105 110  
 Glu Leu Ala Ile Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala  
 115 120 125  
 Ala Met Leu Thr Val Trp Ala Cys Gln Gly Arg Gln Cys Ser Tyr Arg  
 130 135 140  
 Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu Ser Glu Cys Asn Leu  
 145 150 155 160  
 Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Val Thr Ala  
 165 170 175  
 Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala  
 180 185 190  
 Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu  
 195 200 205  
 Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe  
 210 215 220  
 Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln  
 225 230 235 240  
 Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp  
 245 250 255  
 Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr  
 260 265 270  
 His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr  
 275 280 285  
 Val Ala Gly Met Ile Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala  
 290 295 300  
 His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala  
 305 310 315 320  
 His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Glu Thr  
 325 330 335  
 Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Leu  
 340 345 350  
 Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr  
 355 360 365

Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu  
370 375 380

Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu  
385 390 395 400

Ile Ala Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu Tyr Gln Leu  
405 410 415

Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg  
420 425 430

Lys Val Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro Asn Gln Trp  
435 440 445

Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys  
450 455 460

Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys  
465 470 475 480

Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala  
485 490

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 6 and 7 stand for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

His Arg Asp Leu Lys Xaa Xaa Asn  
1 5

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.  
The letter "N" stands for Inosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GARRARGTNG CNGTNAARRT NTT

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.  
The letter "N" stands for Inosine.  
The letter "K" stands for G or T.  
The letter "M" stands for A or C.  
The letter "Y" stands for C or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTRATRTCNC KRTGNGMNAT NGMNGGYTT

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(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 2 stands for Lys or Glu. "Xaa" in position 7 stands for Val or Ile.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Xaa Val Ala Val Lys Xaa Phe  
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 3 stands for Ala or Ser. "Xaa" in position 5 stands for Ala or Ser.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Lys Pro Xaa Ile Xaa His Arg Asp Ile Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AACTTTGGCT GGTATCTGAA TATC

24

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCTTGTGTAC CAACAAATCTC CATA

24

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCCAGAGAT GAGAGATCTT GG

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(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TTCCAGCCAC GGTCACTATG TT

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(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Tyr Arg Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTTCGAAAGC TTGAAATCGG TACCATCGAT TCTAGAGTTA ACTTCGAA

48

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCTAGAACG CGTTAAGGCG CGCCAATATC GATGAATTCT TCGAACG

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